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| (54) Title: NOVEL ENZYME (57) Abstract <p>A protein having luciferase activity and at least 60 % similarity to luciferase from <i>Photinus pyralis</i>, <i>Luciola mingrelica</i>, <i>Luciola cruciata</i> or <i>Luciola lateralis</i>, <i>Hotaria paroula</i>, <i>Pyrophorus plagiophthalmus</i>, <i>Lampyrus noctiluca</i>, <i>Pyrocoelia nayako</i> or <i>Photinus pennsylvanica</i> wherein in the sequence of the enzyme, at least one of (a) the amino acid residue corresponding to residue 214 in <i>Photinus pyralis</i> luciferase; (b) the amino acid residue corresponding to residue 232 in <i>Photinus pyralis</i> luciferase; (c) the amino acid residue corresponding to residue 295 in <i>Photinus pyralis</i> luciferase; (d) the amino acid residue corresponding to acid 14 of <i>Photinus pyralis</i> luciferase; (e) the amino acid residue corresponding to amino acid 35 of <i>Photinus pyralis</i> luciferase; (f) the amino acid residue corresponding to amino acid residue 105 of <i>Photinus pyralis</i> luciferase; (g) the amino acid residue corresponding to amino acid residue 234 of <i>Photinus pyralis</i> luciferase; (h) the amino acid residue corresponding to amino acid residue 420 of <i>Photinus pyralis</i> luciferase; (i) the amino acid residue corresponding to amino acid residue 310 of <i>Photinus pyralis</i> luciferase; is different to the amino acid which appears in the corresponding wild type sequence and wherein the luciferase enzyme has increased thermostability as compared to an enzyme having the amino acid of the corresponding wild-type luciferase at this position.</p> | | |

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Novel Enzyme

The present invention relates to novel proteins, in particular mutant luciferase enzymes having increased thermostability as compared to the corresponding wild type enzyme, to the use of these enzymes in assays and to test kits containing them.

Firefly luciferase catalyses the oxidation of luciferin in the presence of ATP, Mg^{2+} and molecular oxygen with the resultant production of light. This reaction has a quantum yield of about 0.88. The light emitting property has led to its use in a wide variety of luminometric assays where ATP levels are being measured. Examples of such assays include those which are based upon the described in EP-B-680515 and WO 96/02665.

Luciferase is obtainable directly from the bodies of insects, in particular beetles such as fireflies or glow-worms. Particular species from which luciferases have been obtained include the Japanese GENJI or KEIKE fireflies, *Luciola cruciata* and *Luciola lateralis*, the East European firefly *Luciola mingrellica*, the North American firefly *Photinus pyralis* and the glow-worm *Lampyrus noctiluca*. Other species from which luciferase can be obtained are listed in Ye et al., Biochimica et Biophysica Acta, 1339 (1997) 39-52. Yet a further species is *Phrixothrix* (railroad-worms), as described by Viviani et al., Biochemistry, 38, (1999) 8271-8279.

However, since many of the genes encoding these enzymes have been cloned and sequenced, they may also be produced using recombinant DNA technology. Recombinant DNA sequences encoding the enzymes are used to transform microorganisms such as *E. coli* which then express the desired enzyme product.

The heat stability of wild and recombinant type luciferases is such that they lose activity quite rapidly when exposed to temperatures in excess of about 30°C, particularly over 35°C. This instability causes problems when the enzyme is used or stored at high ambient temperature, or if the assay is effected

under high temperature reaction conditions, for example in order to increase reaction rate.

Mutant luciferases having increased thermostability are known
5 from EP-A-524448 and WO95/25798. The first of these describes
a mutant luciferase having a mutation at position 217 in the
Japanese firefly luciferase, in particular by replacing a
threonine residue with an isoleucine residue. The latter
describes mutant luciferases having over 60% similarity to
10 luciferase from *Photinus pyralis*, *Luciola mingrelica*, *Luciola*
cruciata or *Luciola lateralis* but in which the amino acid
residue corresponding to residue 354 of *Photinus pyralis* or 356
of the *Luciola* species is mutated such that it is other than
glutamate.

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The applicants have found yet further mutants which can bring
about increased thermostability and which may complement the
mutations already known in the art.

20 The present invention provides a protein having luciferase
activity and at least 60% similarity to luciferase from
Photinus pyralis, *Luciola mingrelica*, *Luciola cruciata* or
Luciola lateralis, *Hotaria paroula*, *Pyrophorus plagiophthalmus*
Lampyrus noctiluca, *Pyrocoelia nayako*, *Photinus pennsylvanica*
25 or *Phrixothrix*, wherein in the sequence of the enzyme, at least
one of

- (a) the amino acid residue corresponding to residue 214 in
Photinus pyralis luciferase or to residue 216 of *Luciola*
mingrelica, *Luciola cruciata* or *Luciola lateralis* luciferase;
- 30 (b) the amino acid residue corresponding to residue 232 in
Photinus pyralis luciferase or to residue 234 of *Luciola*
mingrelica, *Luciola cruciata* or *Luciola lateralis* luciferase;
- (c) the amino acid residue corresponding to residue 295 in
Photinus pyralis luciferase or to residue 297 of *Luciola*
35 *mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase;
- (d) the amino acid residue corresponding to amino acid 14 of
the *Photinus pyralis* luciferase or to residue 16 of *Luciola*

mingrelica, & residue 17 of *Luciola cruciata* or *Luciola lateralis*;

- (e) the amino acid residue corresponding to amino acid 35 of the *Photinus pyralis* luciferase or to residue 37 of *Luciola mingrelica* 38 of *Luciola cruciata* or *Luciola lateralis*;
- (f) the amino acid residue corresponding to amino acid residue 105 of the *Photinus pyralis* luciferase or to residue 106 of *Luciola mingrelica*, 107 of *Luciola cruciata* or *Luciola lateralis* or 108 of *Luciola lateralis* gene;
- (g) the amino acid residue corresponding to amino acid residue 234 of the *Photinus pyralis* luciferase or to residue 236 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*;
- (h) the amino acid residue corresponding to amino acid residue 420 of the *Photinus pyralis* luciferase or to residue 422 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*;
- (i) the amino acid residue corresponding to amino acid residue 310 of the *Photinus pyralis* luciferase or to residue 312 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*; is different to the amino acid which appears in the corresponding wild type sequence and wherein the luciferase enzyme possesses has increased thermostability as compared to an enzyme having the amino acid of the corresponding wild-type luciferase of a particular species at this position.

- Preferably, the protein has luciferase activity and at least 60% similarity to luciferase from *Photinus pyralis*, *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*, *Hotaria paroula*, *Pyrophorus plagiophthalmus* *Lampyrus noctiluca*, *Pyrocoelia nayako*, or *Photinus pennsylvanica*.

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- In particular, the protein is a recombinant protein which has luciferase activity and substantially the sequence of a wild-type luciferase, for example of *Photinus pyralis*, *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*, *Hotaria paroula*, *Pyrophorus plagiophthalmus* (Green-Luc GR), *Pyrophorus plagiophthalmus* (Yellow-Green Luc YG), *Pyrophorus plagiophthalmus* (Yellow-Luc YE), *Pyrophorus plagiophthalmus*
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(Orange-Luc OR), *Lampyrus noctiluca*, *Pyrocellia nayako* *Photinus pennsylvanica* LY, *Photinus pennsylvanica* KW, *Photinus pennsylvanica* J19, or *Phrixothrix* green (Pv_{GR}) or red (Ph_{RE}) but which may include one or more, for example up to 100 amino acid residues, preferably no more than 50 amino acids and more preferably no more than 30 amino acids, which have been engineered to be different to that of the wild type enzyme.

In particular, bioluminescent enzymes from species that can use the substrate D-luciferin (4,5-dihydro-2-[6-hydroxy-2-benzothiazolyl]-4-thiazole carboxylic acid) to produce light emission may form the basis of the mutant enzymes of the invention.

By way of example, where the protein has substantially the sequence of luciferase of *Photinus pyralis*, in accordance with the invention, at least one of

- (a) the amino acid residue corresponding to residue 214 in *Photinus pyralis* luciferase has been changed to be other than threonine;
- (b) the amino acid residue corresponding to residue 232 in *Photinus pyralis* luciferase has been changed to be other than isoleucine;
- (c) the amino acid residue corresponding to residue 295 in *Photinus pyralis* luciferase has been changed to be other than phenylalanine;
- (d) the amino acid residue corresponding to amino acid 14 of the *Photinus pyralis* luciferase has been changed to be other than phenylalanine;
- (e) the amino acid residue corresponding to amino acid 35 of the *Photinus pyralis* luciferase has been changed to be other than leucine;
- (f) the amino acid residue corresponding to amino acid residue 105 of the *Photinus pyralis* luciferase has been changed to be other than alanine;
- (g) the amino acid residue corresponding to amino acid residue 234 of the *Photinus pyralis* luciferase has been changed to be other than aspartic acid;

(h) the amino acid residue corresponding to amino acid residue 420 of the *Photinus pyralis* luciferase has been changed to be other than serine;

(i) the amino acid residue corresponding to amino acid residue 310 of the *Photinus pyralis* luciferase has been changed to be other than histidine.

Where the protein has substantially the sequence of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* enzyme, in accordance with the invention, at least one of

(a) the amino acid residue corresponding to residue 216 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase is other than glycine (for *Luciola mingrelica* based sequences) or asparagine (for *Luciola cruciata* or *Luciola lateralis*) based sequences;

(b) the amino acid residue corresponding to residue 234 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase is other than serine;

(c) amino acid residue corresponding to residue 297 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase is other than leucine;

(d) amino acid residue corresponding to amino acid 16 of *Luciola mingrelica*, or to amino acid 17 of *Luciola cruciata* or *Luciola lateralis* is other than phenylalanine;

(e) amino acid residue corresponding to residue 37 of *Luciola mingrelica*, or 38 of *Luciola cruciata* or *Luciola lateralis* is other than lysine;

(f) amino acid residue corresponding to amino acid residue 106 of *Luciola mingrelica*, or to amino acid 107 of *Luciola cruciata* or *Luciola lateralis* or to amino acid 108 of *Luciola lateralis* gene is other than glycine;

(g) amino acid residue corresponding to amino acid residue 236 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* is other than glycine;

(h) amino acid residue corresponding to residue 422 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* is other than threonine;

(i) amino acid residue corresponding to amino acid residue 312 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* is other than threonine (for *Luciola mingrelica* based sequences) or valine (for *Luciola cruciata* or *Luciola lateralis*) based sequences.

The particular substituted amino acids in any case which give rise to enhanced thermostability can be determined by routine methods as illustrated hereinafter. In each case, different substitutions may result in enhanced thermostability. Substitution may be effected by site-directed mutagenesis of DNA encoding native or suitable mutant proteins as would be understood by the skilled person. The invention in this case is associated with the identification of the positions which are associated with thermostability.

In general however, it may be desirable to consider substituting an amino acid of different properties to the wild type amino acid. Thus hydrophilic amino acid residues may, in some cases be preferably substituted with hydrophobic amino acid residues and vice versa. Similarly, acidic amino acid residues may be substituted with basic residues.

For instance, the protein may comprise a protein having luciferase activity and at least 60% similarity to luciferase from *Photinus pyralis*, *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* enzyme wherein in the sequence of the enzyme, at least one of

(a) the amino acid residue corresponding to residue 214 in *Photinus pyralis* luciferase and to residue 216 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase is mutated and is other than threonine in the case of *Photinus pyralis* luciferase; or

(b) the amino acid residue corresponding to residue 232 in *Photinus pyralis* luciferase and to residue 234 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase is

mutated and is other than isoleucine in the case of *Photinus pyralis* luciferase; or

(c) amino acid residue corresponding to residue 295 in *Photinus pyralis* luciferase and to residue 297 of *Luciola mingrelia*,

5 *Luciola cruciata* or *Luciola lateralis* luciferase is mutated and is for example, other than phenylalanine in the case of *Photinus pyralis* luciferase;

and the luciferase enzyme has increased thermostability as compared to the wild-type luciferase.

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The sequences of all the various luciferases show that they are highly conserved having a significant degree of similarity between them. This means that corresponding regions among the enzyme sequences are readily determinable by examination of the

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sequences to detect the most similar regions, although if necessary commercially available software (e.g. "Bestfit" from the University of Wisconsin Genetics Computer Group; see Devereux et al (1984) Nucleic Acid Research 12: 387-395) can be used in order to determine corresponding regions or particular amino acids between the various sequences. Alternatively or additionally, corresponding acids can be determined by reference to L. Ye et al., Biochim. Biophys Acta 1339 (1997) 39-52. The numbering system used in this reference forms the basis of the numbering system used in the present application.

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With respect to the possible change of the amino acid residue corresponding to residue 214 in *Photinus pyralis* luciferase, the polar amino acid threonine is suitably replaced with a non polar amino acid such as alanine, glycine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan or cysteine. A particularly preferred substitution for the threonine residue corresponding to residue 214 in *Photinus pyralis* is alanine. A more preferred substitution is cysteine. However, different polar residues such as asparagine at this position may also enhance the thermostability of the corresponding enzyme having threonine at this position.

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Other amino acids which appear at this position in wild-type luciferase enzymes include glycine (*Luciola mingrelica*, *Hotaria paroula*), asparagine (*Pyrophorus plagiophthalmus*, GR, YC, YE and OR, *Luciola cruciata*, *Luciola lateralis*, *Lampyrus noctiluca*, *Pyrocella nayako* *Photinus pennsylvanicus* LY, KW, J19) and serine (position 211 in *Phrixothrix* luciferase). These may advantageously be substituted with non-polar or different non-polar side chains such as alanine and cysteine.

10 As regards the possible change of the amino acid residue corresponding to residue 232 in *Photinus pyralis* luciferase, the nonpolar amino acid isoleucine is suitably replaced with a different non polar amino acid such as alanine, glycine, valine, leucine, proline, phenylalanine, methionine, tryptophan
15 or cysteine. Other amino acids appearing at this position in wild type sequences include serine and asparagine (as well as valine or alanine at corresponding position 229 in *Phritothix* green and red respectively). Suitably, these polar residues are substituted by non-polar residues such as those
20 outlined above. A particularly preferred substitution for the residue corresponding to residue 232 in *Photinus pyralis* luciferase and to residue 234 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase is alanine, where this represents a change of amino acid over the wild-type sequence.

25 Changes of the amino acid residue corresponding to residue 295 in *Photinus pyralis* luciferase and to residue 297 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase, may also affect the thermostability of the protein. (This
30 corresponds to position 292 in *Phrixothrix* luciferase.) In general, the amino acid at this position is a non-polar amino acid phenylalanine or leucine. These are suitably changed for different non-polar amino acids. For example, in *Photinus pyralis*, the non-polar amino acid phenylalanine is suitably
35 replaced with a different non polar amino acid, such as alanine, leucine, glycine, valine, isoleucine, proline, methionine, tryptophan or cysteine. A particularly preferred

substitution for the phenylalanine residue corresponding to residue 214 in *Photinus pyralis* luciferase is leucine.

Mutation at the amino acid residue corresponding to amino acid
5 14 of the *Photinus pyralis* luciferase or to amino acid 16 in
Luciola luciferase, (13 in *Phrixothrix* luciferase) is also
possible. This amino acid residue (which is usually
phenylalanine, but may also be leucine, serine, arginine or in
some instances tyrosine) is suitably changed to a different
10 amino acid, in particular to a different nonpolar amino acid
such as alanine, valine, leucine, isoleucine, proline,
methionine or tryptophan, preferably alanine.

Mutation at the amino acid residue corresponding to amino acid
15 35 of the *Photinus pyralis* luciferase or to amino acid residue
37 in *Luciola mingrelica* luciferase (corresponding to amino
acid 38 in other *Luciola* spp. And in *Phrixothrix*) may also be
effective. This amino acid varies amongst wild type enzymes,
which may include leucine (*Photinus pyralis*) but also lysine,
20 histidine, glycine, alanine, glutamine and aspartic acid at
this position. Suitably the amino residue at this position is
substituted with a non-polar amino acid residue or a different
non-polar amino acid such as
such as alanine, valine, phenylalanine, isoleucine, proline,
25 methionine or tryptophan. A preferred amino acid at this
position is alanine, where this is different to the wild-type
enzyme.

Mutations at the amino acid corresponding to position 14 of the
30 *Photinus pyralis* sequence and/or mutation at the amino acid
residue corresponding to amino acid 35 of the *Photinus pyralis*
luciferase are preferably not the only mutation in the enzyme.
They are suitably accompanied by others of the mutations
defined above, in particular those at positions corresponding
35 to positions 214, 395 or 232 of *Photinus pyralis* luciferase.

Changes of the amino acid residue corresponding to residue 105 in *Photinus pyralis* luciferase and to residue 106 of *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase, (102 in *Phrixothrix*) may also affect the thermostability of the protein. In general, the amino acid at this position is a non-polar amino acid alanine or glycine, or serine in *Phrixothrix*. These are suitably changed for different non-polar amino acids. For example, in *Photinus pyralis*, the non-polar amino acid alanine is suitably replaced with a different non polar amino acid, such as phenylalanine, leucine, glycine, valine, isoleucine, proline, methionine or tryptophan. A particularly preferred substitution for the alanine residue corresponding to residue 105 in *Photinus pyralis* luciferase is valine.

Changes of the amino acid residue corresponding to residue 234 in *Photinus pyralis* luciferase and to residue 236 of *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase (231 in *Phrixothrix*), may also affect the thermostability of the protein. In general, the amino acid at this position is aspartic acid or glycine and in some cases, glutamine or threonine. These are suitably changed for non-polar or different non-polar amino acids as appropriate. For example, in *Photinus pyralis*, the amino acid residue is aspartic acid is suitably replaced with a non polar amino acid, such as alanine, leucine, glycine, valine, isoleucine, proline, methionine or tryptophan. A particularly preferred substitution for the phenylalanine residue corresponding to residue 234 in *Photinus pyralis* luciferase is glycine. Where a non-polar amino acid residue such as glycine is present at this position (for example in *Luciola* luciferase), this may be substituted with a different non-polar amino acid.

Changes of the amino acid residue corresponding to residue 420 in *Photinus pyralis* luciferase and to residue 422 of *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase (417 in *Phrixothrix* green and 418 in *Phrixothrix* red), may also affect the thermostability of the protein. In general, the

amino acid at this position is an uncharged polar amino acid serine or threonine or glycine. These are suitably changed for different uncharged polar amino acids. For example, in *Photinus pyralis*, the serine may be replaced with asparagine, glutamine, threonine or tyrosine, and in particular threonine.

Changes of the amino acid residue corresponding to residue 310 in *Photinus pyralis* luciferase and to residue 312 of *Luciola mingrelia*, *Luciola cruciata* or *Luciola lateralis* luciferase, may also affect the thermostability of the protein. The amino acid residue at this position varies amongst the known luciferase proteins, being histidine in *Photinus pyralis*, *Pyrocellia nayako*, *Lampyrus noctiluca* and some forms of *Photinus pennsylvanicus* luciferase, threonine in *Luciola mingrelia*, *Hotaria paroula* and *Phrixothrix* (where it is amino acid 307) luciferase, valine in *Luciola cruciata* and *Luciola lateralis*, and asparagine in some *Pyrophorus plagiophthalmus* luciferase. Thus, in general, the amino acid at this position is hydrophilic amino acid which may be changed for a different amino acid residue which increases thermostability of the enzyme. A particularly preferred substitution for the histidine residue corresponding to residue 310 in *Photinus pyralis* luciferase is arginine.

Other mutations may also be present in the enzyme. For example, in a preferred embodiment, the protein also has the amino acid at position corresponding to amino acid 354 of the *Photinus pyralis* luciferase (356 in *Luciola* luciferase and 351 in *Phrixothrix*) changed from glutamate, in particular to an amino acid other than glycine, proline or aspartic acid. Suitably, the amino acid at this position is tryptophan, valine, leucine, isoleucine are asparagine, but most preferably is lysine or arginine. This mutation is described in WO 95/25798.

In an alternative preferred embodiment, the protein also has the amino acid at the position corresponding to amino acid 217

in *Luciola luciferase* (215 in *Photinus pyralis*) changed to a hydrophobic amino acid in particular to isoleucine, leucine or valine as described in EP-A-052448.

5 The proteins may contain further mutations in the sequence provided the luciferase activity of the protein is not unduly compromised. The mutations suitably enhance the properties of the enzyme or better suit it for the intended purpose in some way. This may mean that they result in enhanced
10 thermostability and/or colour shift properties, and/or the K_m for ATP of the enzymes. Examples of mutations which give rise to colour shifts are described in WO95/18853. Mutations which affect K_m values are described for example in WO 96/22376 and International Patent Application No. PCT/GB98/01026 which are
15 incorporated herein by reference.

Proteins of the invention suitably have more than one such mutation, and preferably all three of the mutations described above.

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Proteins of the invention include both wild-type and recombinant luciferase enzymes. They have at least 60% similarity to the sequences of *Photinus pyralis*, *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* or other
25 luciferase enzymes as discussed above in the sense that at least 60% of the amino acids present in the wild-type enzymes are present in the proteins of the invention. Such proteins can have a greater degree of similarity, in particular at least 70%, more preferably at least 80% and most preferably at least
30 90% to the wild-type enzymes listed above. Similar proteins of this type include allelic variants, proteins from other insect species as well as recombinantly produced enzymes.

They may be identified for example, in that they are encoded by
35 nucleic acids which hybridise with sequences which encode wild-type enzymes under stringent hybridisation conditions, preferably high stringency conditions. Such conditions would be well understood by the person skilled in the art, and are

exemplified for example in Sambrook et al. (1989) Molecular Cloning, Cold Spring Harbor Laboratory Press). In general terms, low stringency conditions can be defined as 3 x SSC at about ambient temperature to about 65°C, and high stringency
5 conditions as 0.1 x SSC at about 65°C. SSC is the name of a buffer of 0.15M NaCl, 0.015M trisodium citrate. 3 x SSC is three times as strong as SSC and so on.

In particular, the similarity of a particular sequence to the
10 sequences of the invention may be assessed using the multiple alignment method described by Lipman and Pearson, (Lipman, D.J. & Pearson, W.R. (1985) Rapid and Sensitive Protein Similarity Searches, Science, vol 227, pp1435-1441). The "optimised" percentage score should be calculated with the following
15 parameters for the Lipman-Pearson algorithm: ktup =1, gap penalty =4 and gap penalty length =12. The sequence for which similarity is to be assessed should be used as the "test sequence" which means that the base sequence for the comparison, such as the sequence of *Photinus pyralis* or any of
20 the other sequences listed above, as recorded in Ye et al., supra., or in the case of *Phrixotrix*, as described in Biochemistry, 1999, 38, 8271-8279, should be entered first into the algorithm. Generally, *Photinus pyralis* will be used as the reference sequence.

25 Particular examples of proteins of the invention are wild-type luciferase sequence with the mutations as outlined above. The proteins have at least one and preferably more than one such mutation.

30 The invention further provides nucleic acids which encode the luciferases as described above. Suitably, the nucleic acids are based upon wild-type sequences which are well known in the art. Suitable mutation to effect the desired mutation in the amino
35 acid sequence would be readily apparent, based upon a knowledge of the genetic code.

The nucleic acids of the invention are suitably incorporated into an expression vector such as a plasmid under the control of control elements such as promoters, enhancers, terminators etc. These vectors can then be used to transform a host cell, for example a prokaryotic or eukaryotic cell such as a plant or animal cell, but in particular a prokaryotic cell such as *E. coli* so that the cell expresses the desired luciferase enzyme. Culture of the thus transformed cells using conditions which are well known in the art will result in the production of the luciferase enzyme which can then be separated from the culture medium. Where the cells are plant or animal cells, plants or animals may be propagated from said cells. The protein may then be extracted from the plants, or in the case of transgenic animals, the proteins may be recovered from milk. Vectors, transformed cells, transgenic plants and animals and methods of producing enzyme by culturing these cells all form further aspects of the invention.

The *Photinus pyralis* T214A mutant luciferase was created by random mutagenesis as described hereinafter. It was found that the T214A single point mutation has greater thermostability than wild type luciferase.

Two new triple mutant luciferases: E354K/T214A/A215L and E354K/T214A/I232A were also prepared and these also have exhibited greater thermostability.

Particular examples of mutant enzymes of *Photinus pyralis* which fall within the scope of the invention include the following:

I232A/E354K
T214A/I232A/E354K
A215L/I232A/E354K
T214A/I232A/E354K/A215L
I232A/E354K/T214A/F295L
I232A/E354K/T214A F295L/F14A/L35A
I232A/E354K/T214A/F295L/F14A/L35A/A215L
A105V
T214A

T214C

T214N

T295L

I232A

5 F14A

L35A

D234G

S420T

H310R

10 or equivalents of any of these when derived from the
luciferases of other species.

The mutations for the creation of the triple mutant were
introduced to the luciferase gene on plasmid pET23 by site-
15 directed mutagenesis, (PCR). The oligonucleotides added to the
PCR reaction in order to effect the relevant mutations are
given in the Examples below.

It has been reported previously that the effect of point
20 mutations at the 354 and 215 positions are additive. This
invention provides the possibility of combining three or more
such mutations to provide still greater thermostability.

Thermostable luciferase of the invention will advantageously be
25 employed in any bioluminescent assay which utilises the
luciferase/luciferin reaction as a signalling means. There are
many such assays known in the literature. The proteins may
therefore be included in kits prepared with a view to
performing such assays, optionally with luciferin and any other
30 reagents required to perform the particular assay.

The invention will now be particularly described by way of
example with reference to the accompanying diagrammatic
drawings in which:

35

Figure 1 illustrates the plasmids used in the production of
mutants in accordance with the invention;

Figure 2 shows the results of heat inactivation studies on luciferases including luciferases of the invention;

Figure 3 shows the results of thermostability experiments on
5 various luciferase mutants;

Figure 4 shows the results of thermostability experiments on other luciferase mutants; and

10 Figure 5 shows oligonucleotides used in the preparation of mutant enzymes of the invention.

Example 1

Identification of Thermostable Mutant Luciferase

15 The error-prone PCR was based on the protocol devised by Fromant et al., Analytical Biochemistry, 224, 347-353 (1995).

The dNTP mix in this reaction was:

35mM dTTP
20 12.5mM dGTP
22.5mM dCTP
14mM dATP

The PCR conditions were:

25 0.5 μ l (50ng) plasmid pPW601a J54*
5.0 μ l 10x KCl reaction buffer
1 μ l each of W56 and W57* (60 pmoles of each primer)
1 μ l Biotaq TM polymerase (5U)
30 2 μ l dNTPs (see above)
1.76 μ l MgCl₂ (50 mM stock)
1 μ l mNCl₂ (25mM stock) [final concentration in reaction = 3.26mM]
36.7 μ l dH₂O

35 *Plasmid pPW601aJ54 is a mutated version of pPW601a (WO 95/25798) where an NdeI site has been created within the 3

bases prior to the ATG start codon. This allows for easy cloning from pPW601a into the pET23 vector.

+Primer sequences:

5 W56:

5' - AAACAGGGACCCATATGGAAGACGC - 3'

W57:

5' - AATTAACTCGAGGAATTCGTCATCGCTGAATACAG - 3')

10 Cycling parameters were:

94°C-5 min

Then 12 x cycles of: 94°C-30s

55°C-30s

15 72°C-5min

72°C-10 min

The PCR products were purified from the reaction mix using a Clontech Advantage TM PCR-pure kit. An aliquot of the purified
20 products was then digested with the restriction enzymes NdeI and XhoI. The digested PCR products were then "cleaned up" with the Advantage kit and ligated into the vector pET23a which had been digested with the same enzymes.

25 Ligation conditions:

4µl pET23a (56ng)

5µl PCR products (200ng)

3µl 5x Gibco BRL ligase reaction buffer

30 1µl Gibco BRL ligase (10U)

2µl dH₂O

The ligation was carried out overnight at 16°C.

The ligated DNAs were then purified using the Advantage™ kit and then electroporated into electrocompetent *E. coli* HB101 cells (1mm cuvettes, 1.8 Kv).

- 5 Eleven electroporations were performed and the cells were then added to 40 ml of TY broth containing 50µg/ml ampicillin. The cells were then grown overnight at 37°C. The entire 50ml of culture grown overnight was used to purify plasmid DNA. This is the library.

10

Screening the library

An aliquot of the plasmid library was used to electroporate *E. coli* BL21 DE3 cells. These cells were then plated onto LB agar containing 50µg/ml ampicillin and grown overnight at 37°C.

15

- The next day, colonies were picked and patched onto nylon filters on LB agar + amp plates and growth continued overnight at 37°C. The next day, filters were overlaid with a solution of luciferin - 500µM in 100mM sodium citrate pH5.0. The patches were then viewed in a darkroom. One colony/patch was picked from 200 for further analysis.

20

Characterisation of the thermostable mutant

The *E. coli* clone harbouring the mutant plasmid was isolated.

- 25 Plasmid DNA was prepared for ABI sequencing. The entire open reading frame encoding luciferase was sequenced using 4 different oligonucleotide primers. Sequencing revealed a single point mutation at nt 640 (A → G). Giving a codon change of ACT (T) to GCT (A) at amino acid position 214.

30

Example 2

Preparation of Triple Mutant Enzyme

- A mutagenic oligonucleotide was then used to create this same mutation in pMOD1 (A215L/E354K) to create a triple mutant pMOD2 (A215L/E354K/T214A). This mutation also creates a unique SacI/SstI site in pMOD1.

35

Example 3

Preparation of further triple mutant enzyme

The following primers were used to create the triple mutant T214A/I232A/E354K using a standard PCR reaction and with the pET23 plasmid with the T214A mutation as template:

| | |
|------------------------|-----------------|
| CTGATTACACCCAAGGGGGATG | E354K-sense |
| CATCCCCCTTGGGTGTAATCAG | E354K-antisense |

10 GCAATCAAATCGCTCCGGATACTGC I232A-sense
GCAGTATCCGGAGCGATTTGATTGC I232A-antisense.

Example 4

Identification of thermostable 295 mutant

15 The F295 mutant was created using the error-prone PCR method described by Fromant et al., *Analytical Biochemistry*, vol 224, 347-353 (1995). The PCR conditions used were as follows:

0.5 µl (50 ng) plasmid pET23
20 5.0 µl 10x KCI reaction buffer
1 µl primer 1 - 60 pmoles of each primer
1 µl primer 2
1 µl Biotaq™ polymerase (5U)
2 µl dNTPs, in mixture 35 mM dTTP, 12.5 mM dGTP, 22.5 mM dCTP,
25 14 mM dATP
1.76 µl MgCl₂ (50 mM stock)
1 µl MnCl₂ (25 mM stock) [final concentration in reaction = 3.26
mM]
36.7 µl dH₂O
30 Primer 1 = 5' - AAACAGGGACCCATATGGAAGACGC - 3'
Primer 2 = 5' - AATTAAC TCGAGGAATTTTCGTCATCGCTGAATACAG - 3'

The cycling parameters were:

94°C for 5 min

35 15 cycles of: 30 s @ 94°C

30 s @ 55°C

5 min @ 72°C

then 10 min at 72°C

The PCR products were purified from the reaction mix using a Clontech Advantage™ PCR-Pure kit. An aliquot of the purified products was then digested with the restriction enzymes NdeI and XhoI. The digested PCR products were then "cleaned up" with the Advantage™ kit and ligated into the vector pET23a, which had been digested with the same enzymes.

The ligation conditions were as follows:

56 ng pET23a
200 ng PCR products
3 µl 5x Gibco BRL ligase reaction buffer
1µl Gibco BRL ligase (10U)
volume made up to 10 µl with dH₂O

The ligation was carried out overnight at 16°C.

The ligated DNAs were then purified using the Advantage™ kit and then electroporated into electrocompetent *Escherichia coli* DH5α cells (1mm cuvettes, 1.8kV). 1ml of SOC broth was added to each electroporation and the cells allowed to recover and express antibiotic resistance genes encoded by the plasmid. Aliquots of the library were inoculated onto LB agar containing 50 µg/ml ampicillin and the bacteria were grown overnight at 37°C. Nylon filter discs were then overlaid onto the agar plates and the colonies transferred to fresh plates. The original plates were left at room temperature for the colonies to re-grow. The plates with the nylon filters were incubated at 42°C for 2 h before plates were sprayed with 500µM luciferin in 100mM citrate buffer pH5.0 and viewed in a darkroom.

Three thermostable colonies were selected on the basis that they still glowed after 2 h at 42°C. Plasmid DNA was isolated from these clones and sequenced, and this revealed the F295L mutation in each case.

Example 5

Other mutants of the invention were produced by PCR using appropriate combinations of the oligonucleotides listed above as well as the following:

5

GAAAGGCCCGGCACCAGCCTATCCTCTAGAGG F14A-sense
CCTCTAGCGGATAGGCTGGTGCCGGGCCTTTC F14A-antisense

GAGATACGCCGCGGTTCTTGG L35A-sense
10 CCAGGAACCGCGGCGTATCTC L35A-antisense

Example 6Purification of luciferase and heat inactivation studies.

Cells expressing the recombinant mutant luciferases were
15 cultured, disrupted and extracted as described in WO 95/25798
to yield cell free extracts of luciferase.

Eppendorf tubes containing the cell free extracts were
incubated generally at 40°C unless otherwise stated. Purified
20 preparations of wild type luciferases (for comparative purposes
were incubated in thermostability buffer comprising 50mM
potassium phosphate buffer pH7.8 containing 10% saturated
ammonium sulphate, 1mM dithiothreitol and 0.2% bovine serum
albumin (BSA). At set times a tube was removed and cooled in
25 an ice/water bath prior to assay with remaining assayed
activity being calculated as a percentage of the initial
activity or relative bioluminesce.

The results are illustrated in Figures 2 and 3 hereinafter. It
30 can be seen from Figure 2 that luciferase mutants of the
invention have improved thermostability compared with the
previously known mutants.

The dramatic increase in stability over wild-type luciferase
35 (RWT) is clear from Figure 3.

Example 7Investigations into the activity of 214 mutants

A library of 214 mutants was prepared using site-directed mutagenesis using cassette oligos (Figure 5) and thermostable mutants selected and tested as described in Example 1. Three particularly thermostable mutants were characterised by sequencing as described in Example 1 as T214A, T214C and T214N.

O/N cultures of E. coli XL1-Blue harbouring plasmids encoding T214, T214A, T214C and T214N were lysed using the Promega lysis buffer. 50µl of liquid extracts were then heat inactivated at 37°C and 40°C over various time points. Aliquots 10µl of heated extract were then tested in the Promega live assay buffer (100µl).

15

The results are shown in the following Tables

| | 0 | 4 min | 8 min | 22 min | (37°C) |
|----------|--------|-------|-------|--------|--------|
| rwT T214 | 11074 | 5561 | 2555 | 343 | RLU |
| T214C | 106449 | 92471 | 90515 | 78816 | RLU |
| T214A | 63829 | 52017 | 45864 | 35889 | RLU |
| T214N | 60679 | 49144 | 41736 | 29488 | RLU |

| | | % remaining activity 37°C | | |
|----------|-----|---------------------------|------|------|
| rwT T214 | 100 | 50.2 | 23.1 | 3.1 |
| T214C | 100 | 86.9 | 85.0 | 74.0 |
| T214A | 100 | 81.5 | 71.8 | 56.2 |
| T214N | 100 | 81.0 | 68.8 | 48.6 |

20

The experiment was repeated at 40°C with the 3 mutants

| | 0 | 4 min | 8 min | 16 min | |
|-------|--------|-------|-------|--------|-----|
| T214C | 104830 | 79365 | 72088 | 56863 | RLU |
| T214A | 64187 | 43521 | 28691 | 14547 | RLU |
| T214N | 60938 | 38359 | 25100 | 12835 | RLU |

| | | % remaining activity 40°C | | |
|-------|-----|---------------------------|-------|--------|
| | 0 | 4 min | 8 min | 16 min |
| T214C | 100 | 73.7 | 68.8 | 54.2 |
| T214A | 100 | 67.8 | 44.7 | 22.7 |
| T214N | 100 | 63.0 | 41.2 | 21.1 |

These results indicate that T214C is significantly more thermostable than either r-wt or T214A or N. This change in properties is unexpected as it is usually expected that the more cysteine residues that are present, the worse the thermostability.

Example 8

Investigation of other point mutations

A series of other *Photinus pyralis* mutants with single point mutations were prepared using random error-prone PCR (Figure 5). Following, screening and sequencing of the mutants generated, the sequencing was checked using site-directed mutagenesis followed by further sequencing. These were D234G, A105V and F295L. The thermostability of these mutants as well as recombinant wild-type *Photinus pyralis* luciferase was tested. Protein samples in Promega lysis buffer were incubated at 37°C for 10 minutes and their activity assayed after 2, 5 and 10 minutes. The results, showing that each mutation produced enhanced thermostability over wild type, is shown in Figure 4.

Claims

1. A protein having luciferase activity and at least 60% similarity to luciferase from *Photinus pyralis*, *Luciola mingrelica*, *Luciola cruciata*, *Luciola lateralis*, *Hotaria paroula*, *Pyrophorus plagiophthalmus*, *Lampyris noctiluca*, *Pyrocoelia nayako* or *Photinus pennsylvanicus*, wherein in the sequence of the enzyme, at least one of
- 5 (a) the amino acid residue corresponding to residue 214 in *Photinus pyralis* luciferase or to residue 216 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase;
- 10 (b) the amino acid residue corresponding to residue 232 in *Photinus pyralis* luciferase or to residue 234 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase;
- 15 (c) amino acid residue corresponding to residue 295 in *Photinus pyralis* luciferase or to residue 297 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase;
- (d) amino acid residue corresponding to amino acid 14 of the *Photinus pyralis* luciferase or to residue 16 of *Luciola*
- 20 *mingrelica*, or 17 of *Luciola cruciata* or *Luciola lateralis*;
- (e) amino acid residue corresponding to amino acid 35 of the *Photinus pyralis* luciferase or to residue 37 of *Luciola mingrelica*, or 38 of *Luciola cruciata* or *Luciola lateralis*;
- (f) the amino acid residue corresponding to amino acid residue
- 25 105 of the *Photinus pyralis* luciferase or to residue 106 of *Luciola mingrelica*, 107 of *Luciola cruciata* or *Luciola lateralis* or 108 of *Luciola lateralis* gene;
- (g) amino acid residue corresponding to amino acid residue 234 of the *Photinus pyralis* luciferase or to residue 236 of *Luciola*
- 30 *mingrelica*, *Luciola cruciata* or *Luciola lateralis*;
- (h) amino acid residue corresponding to amino acid residue 420 of the *Photinus pyralis* luciferase or to residue 422 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*;
- (i) amino acid residue corresponding to amino acid residue 310
- 35 of the *Photinus pyralis* luciferase or to residue 312 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis*;

is different to the amino acid which appears in the corresponding wild type sequence and wherein the luciferase enzyme has increased thermostability as compared to an enzyme having the amino acid of the corresponding wild-type luciferase at this position.

2. A protein according to claim 1 which has the sequence of a wild-type luciferase, in which more than one amino acid residue is different to that of the wild type enzyme.

10

3. A protein according to claim 2 wherein up to 50 amino acids are different to that of the wild type enzyme.

4. A protein according to any one of the preceding claims wherein the luciferase is a modified form of luciferase of *Photinus pyralis*, *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* luciferase.

5. A protein according to any one of the preceding claims wherein the sequence of luciferase of *Photinus pyralis*, wherein at least one of

- (a) the amino acid residue corresponding to residue 214 in *Photinus pyralis* luciferase is other than threonine;
- (b) the amino acid residue corresponding to residue 232 in *Photinus pyralis* luciferase is other than isoleucine;
- (c) amino acid residue corresponding to residue 295 in *Photinus pyralis* luciferase is other than phenylalanine;
- (d) amino acid residue corresponding to amino acid 14 of the *Photinus pyralis* luciferase is other than phenylalanine;
- (e) amino acid residue corresponding to amino acid 35 of the *Photinus pyralis* luciferase is other than leucine;
- (f) amino acid residue corresponding to amino acid residue 105 of the *Photinus pyralis* luciferase is other than alanine;
- (g) amino acid residue corresponding to amino acid residue 234 of the *Photinus pyralis* luciferase is other than aspartic acid;
- (h) amino acid residue corresponding to amino acid residue 420 of the *Photinus pyralis* luciferase is other than serine;

(i) amino acid residue corresponding to amino acid residue 310 of the *Photinus pyralis* luciferase is other than histidine.

6. A protein according to any one of claims 1 to 4 wherein
5 protein has substantially the sequence of *Luciola mingrelica*,
Luciola cruciata or *Luciola lateralis* enzyme, and wherein at
least one of
- (a) the amino acid residue corresponding to residue 216 of
Luciola mingrelica, *Luciola cruciata* or *Luciola lateralis*
10 luciferase is other than glycine (for *Luciola mingrelica* based
sequences) or asparagine (for *Luciola cruciata* or *Luciola*
lateralis) based sequences;
 - (b) the amino acid residue corresponding to residue 234 of
Luciola mingrelica, *Luciola cruciata* or *Luciola lateralis*
15 luciferase is other than serine;
 - (c) amino acid residue corresponding to residue 297 of *Luciola*
mingrelica, *Luciola cruciata* or *Luciola lateralis* luciferase is
other than leucine;
 - (d) amino acid residue corresponding to amino acid 16 of
20 *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* is
other than phenylalanine;
 - (e) amino acid residue corresponding to residue 37 of *Luciola*
mingrelica, or residue 38 of *Luciola cruciata* and *Luciola*
lateralis is other than lysine;
 - 25 (f) amino acid residue corresponding to amino acid residue 106
of *Luciola mingrelica*, 107 of *Luciola cruciata* or *Luciola*
lateralis, or 108 of *Luciola lateralis* gene is other than
glycine;
 - (g) amino acid residue corresponding to amino acid residue 236
30 of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* is
other than glycine;
 - (h) amino acid residue corresponding to residue 422 of *Luciola*
mingrelica, *Luciola cruciata* or *Luciola lateralis* is other than
threonine;
 - 35 (i) amino acid residue corresponding to amino acid residue 312
of *Luciola mingrelica*, *Luciola cruciata* or *Luciola lateralis* is
other than threonine (for *Luciola mingrelica* based sequences)

or valine (for *Luciola cruciata* or *Luciola lateralis*) based sequences.

7. A protein according to any one of the preceding claims
5 wherein comprising a protein having luciferase activity and at least 60% similarity to luciferase from *Photinus pyralis*, *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* enzyme wherein in the sequence of the enzyme, at least one of (a) the amino acid residue corresponding to residue 214 in
10 *Photinus pyralis* luciferase and to residue 216 of *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase is mutated and is other than threonine in the case of *Photinus pyralis* luciferase; or
(b) the amino acid residue corresponding to residue 232 in
15 *Photinus pyralis* luciferase and to residue 234 of *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase is mutated and is other than isoleucine in the case of *Photinus pyralis* luciferase; or
(c) amino acid residue corresponding to residue 295 in *Photinus*
20 *pyralis* luciferase and to residue 297 of *Luciola mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase is mutated and is for example, other than phenylalanine in the case of *Photinus pyralis* luciferase;
and the luciferase enzyme has increased thermostability as
25 compared to the wild-type luciferase.

8. A protein according to claim 1 wherein the amino acid residue corresponding to residue 214 in *Photinus pyralis* luciferase and to residue 216 of *Luciola mingrellica*, *Luciola*
30 *cruciata* or *Luciola lateralis* luciferase is alanine.

9. A protein according to any one of the preceding claims wherein the amino acid residue corresponding to residue 232 in *Photinus pyralis* luciferase and to residue 234 of *Luciola*
35 *mingrellica*, *Luciola cruciata* or *Luciola lateralis* luciferase is alanine.

10. A protein according to any one of the preceding claims which is a mutated *Photinus pyralis* luciferase wherein the amino acid residue corresponding to residue 295 in *Photinus pyralis* luciferase is leucine.

5

11. A protein according to any one of the preceding claims wherein the amino acid residue corresponding to amino acid 14 of the *Photinus pyralis* luciferase or to amino acid 16 in *Luciola* luciferase, is alanine.

10

12. A protein according to any one of the preceding claims wherein the luciferase is a mutated luciferase of *Photinus pyralis* or a *Luciola* species where the amino acid residue corresponding to amino acid 35 of the *Photinus pyralis*

15 luciferase or to amino acid residue 37 in *Luciola mingrelica* or 38 of *Luciola lateralis* or *cruciata* luciferase is alanine.

13. A protein according to any one of the preceding claims wherein the amino acid residue corresponding to residue 105 in
20 *Photinus pyralis* luciferase and to residue 106 of *Luciola mingrelica*, 107 of *Luciola cruciata* or *Luciola lateralis* or 108 of *Luciola lateralis* gene luciferase is valine.

14. A protein according to any one of the preceding claims
25 which comprises a mutated *Photinus pyralis* luciferase wherein the amino acid residue corresponding to residue 234 in *Photinus pyralis* luciferase is glycine.

15. A protein according to any one of the preceding claims
30 which comprises a mutated *Photinus pyralis* luciferase wherein the amino acid residue corresponding to residue 420 in *Photinus pyralis* luciferase is threonine.

16. A protein according to any one of the preceding claims
35 which comprises a mutated *Photinus pyralis* luciferase wherein the amino acid residue corresponding to residue 310 in *Photinus pyralis* luciferase is arginine.

17. A protein according to any one of the preceding claims wherein the amino acid at position corresponding to amino acid 354 of the *Photinus pyralis* luciferase (356 in *Luciola* luciferase) is other than glutamate.

5

18. A protein according to claim 17 wherein the amino acid at position corresponding to amino acid 354 of the *Photinus pyralis* luciferase (356 in *Luciola* luciferase) is lysine or arginine.

10

19. A protein according to any one of the preceding claims wherein the amino acid at the position corresponding to amino acid 217 in *Luciola* luciferase (215 in *Photinus pyralis*) is a different hydrophobic amino acid.

15

20. A protein according to claim 19 wherein the amino acid at the position corresponding to amino acid 217 in *Luciola* luciferase (215 in *Photinus pyralis*) is isoleucine, leucine or valine.

20

21. A nucleic acid which encodes a luciferase according to any one of the preceding claims.

22. A vector comprising a nucleic acid according to claim 21.

25

23. A cell transformed with a vector according to claim 22.

24. A cell according to claim 23 which is a prokaryotic cell.

30

25. A cell according to claim 23 which is a plant cell.

26. A plant comprising cells according to claim 25.

27. A method of producing a protein according to any one of claims 1 to 20, which method comprises culture of a cell according to claim 23 or growth of a plant according to claim 26.

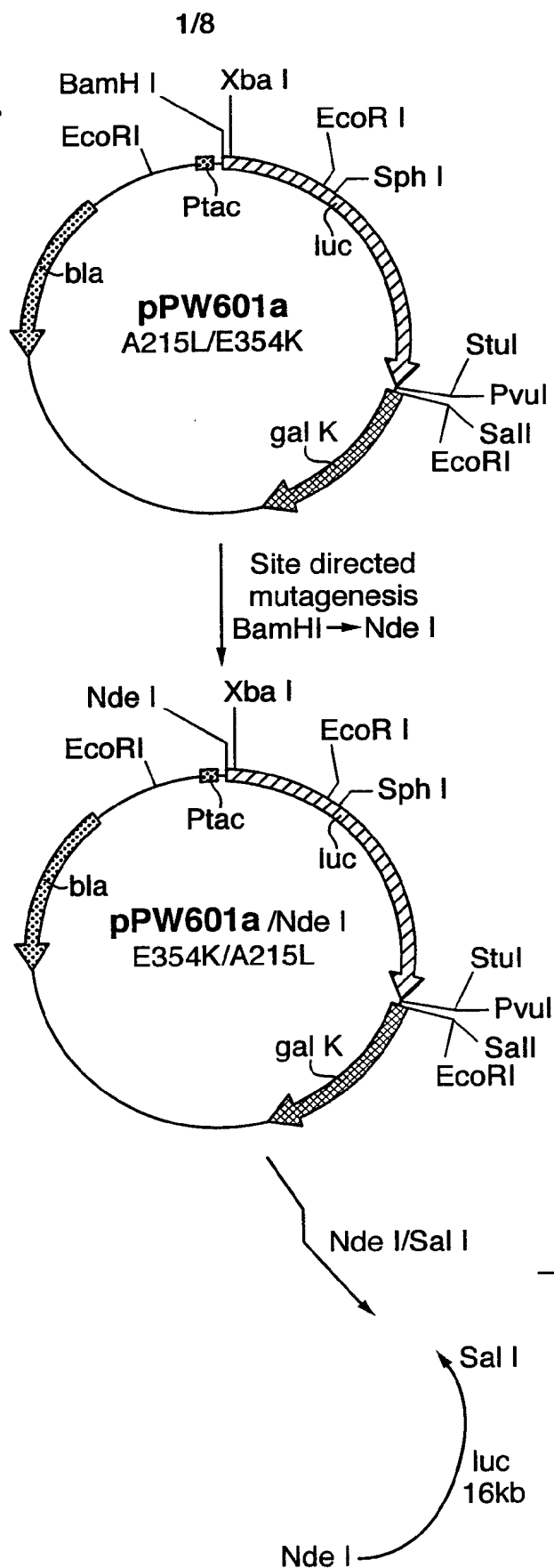
35

28. The use of a protein according to any one of claims 1 to 20 in a bioluminescent assay.

29. A kit comprising a protein according to any one of claims
5 1 to 20.

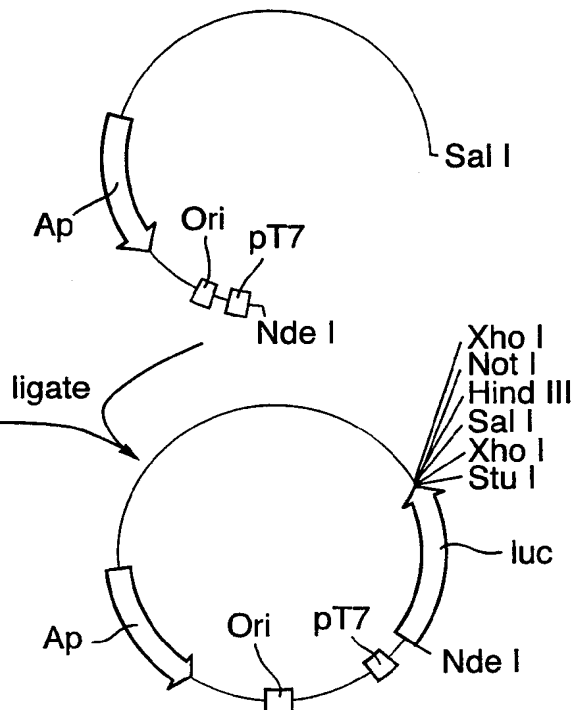
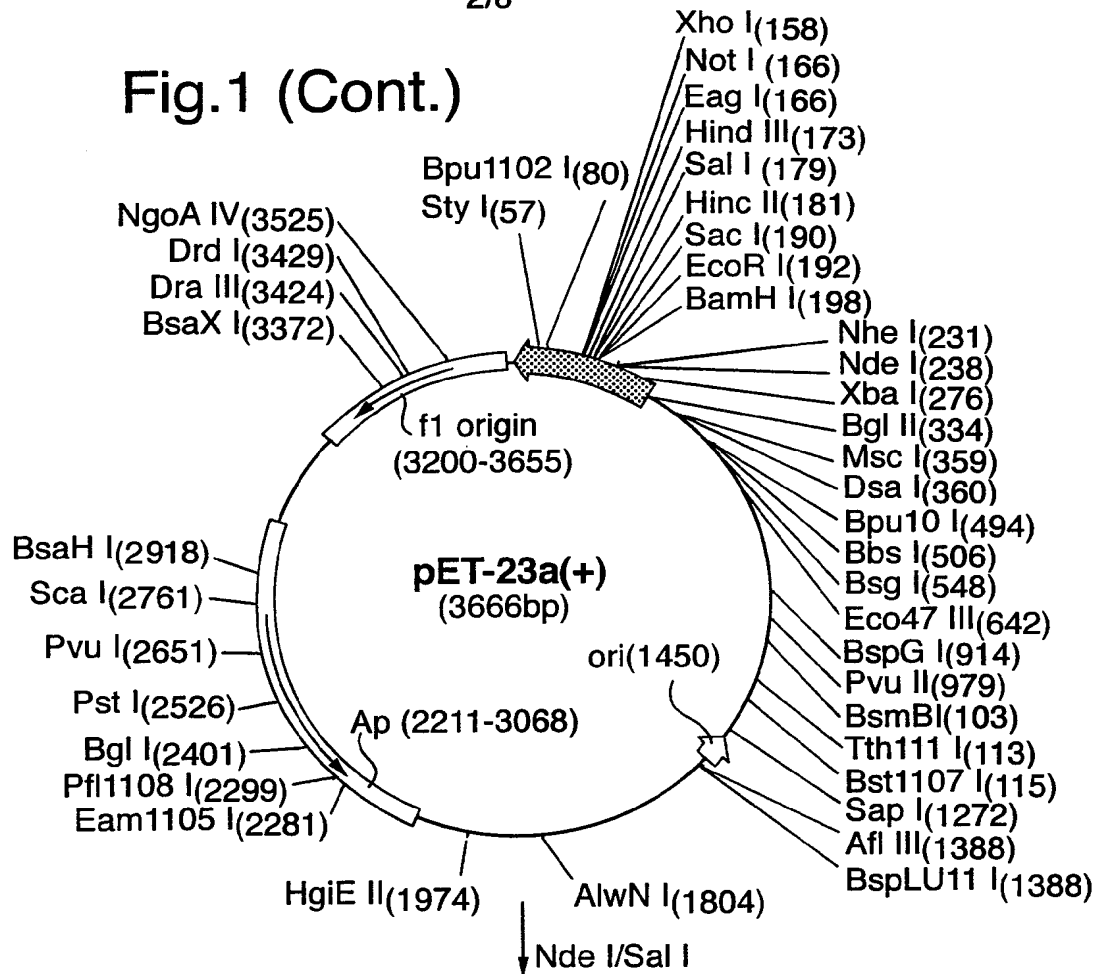
30. A kit according to claim 29 which further comprises luciferin.

Fig.1.



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Fig.1 (Cont.)



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Fig.2.

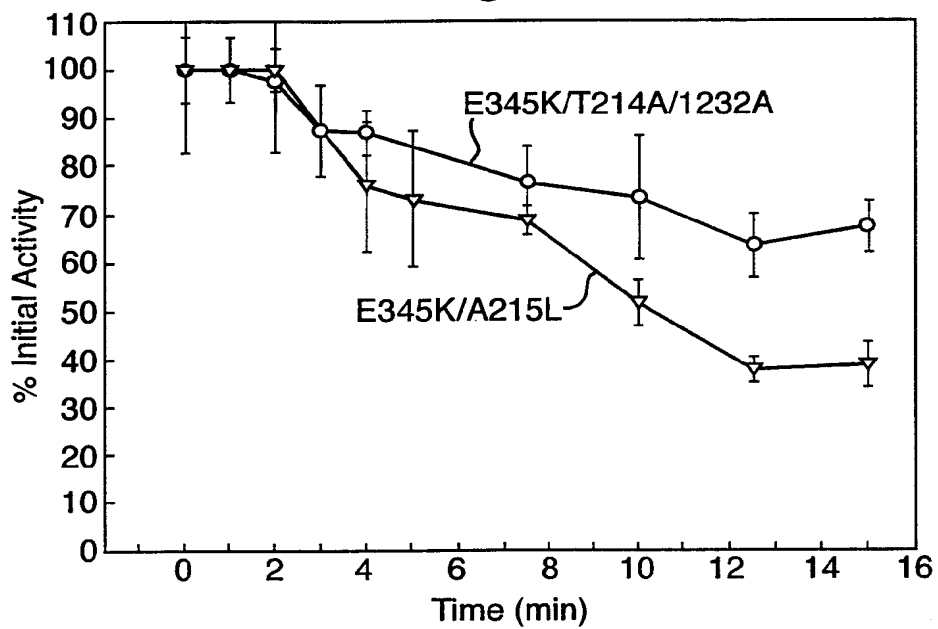


Fig.4.

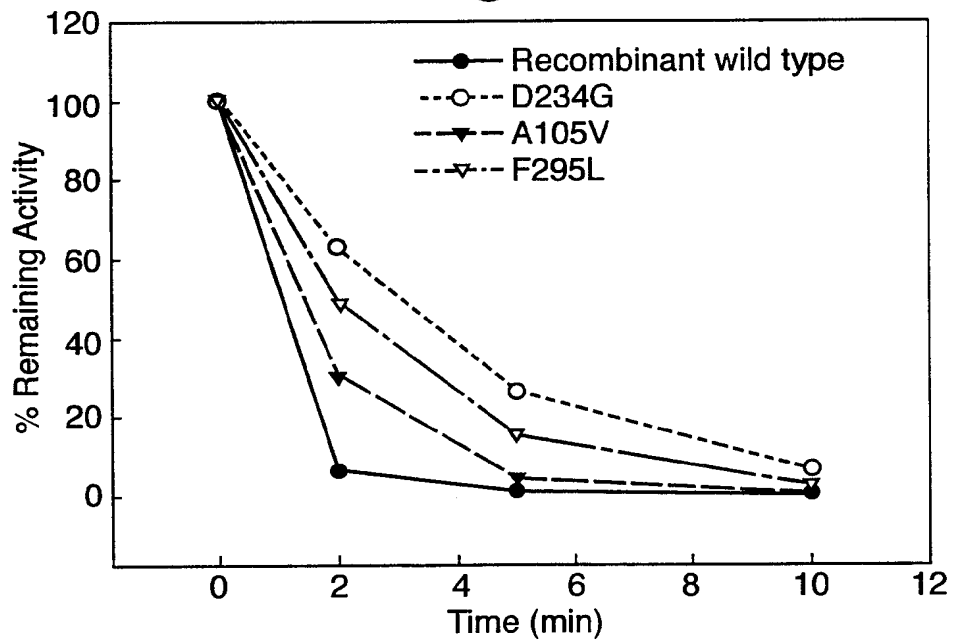


Fig.3a.

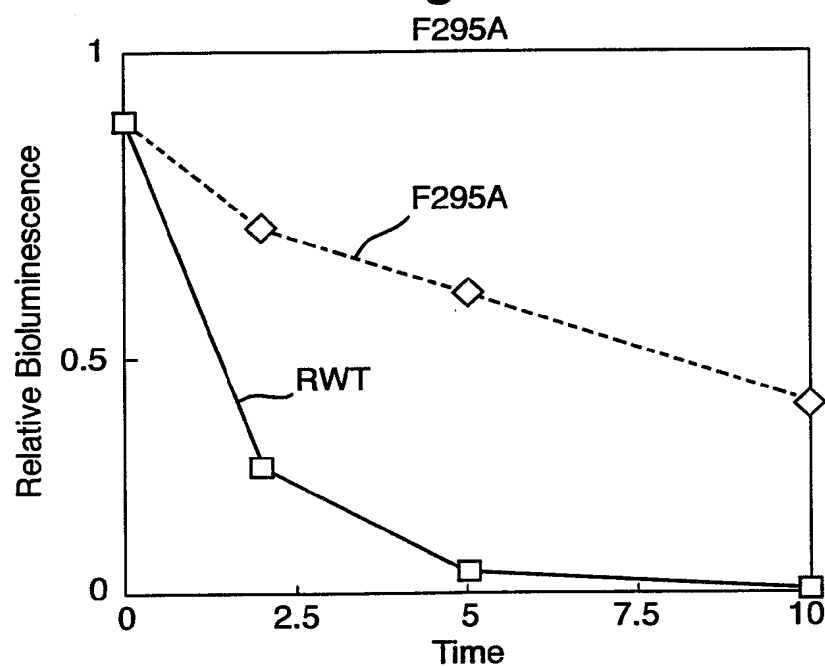
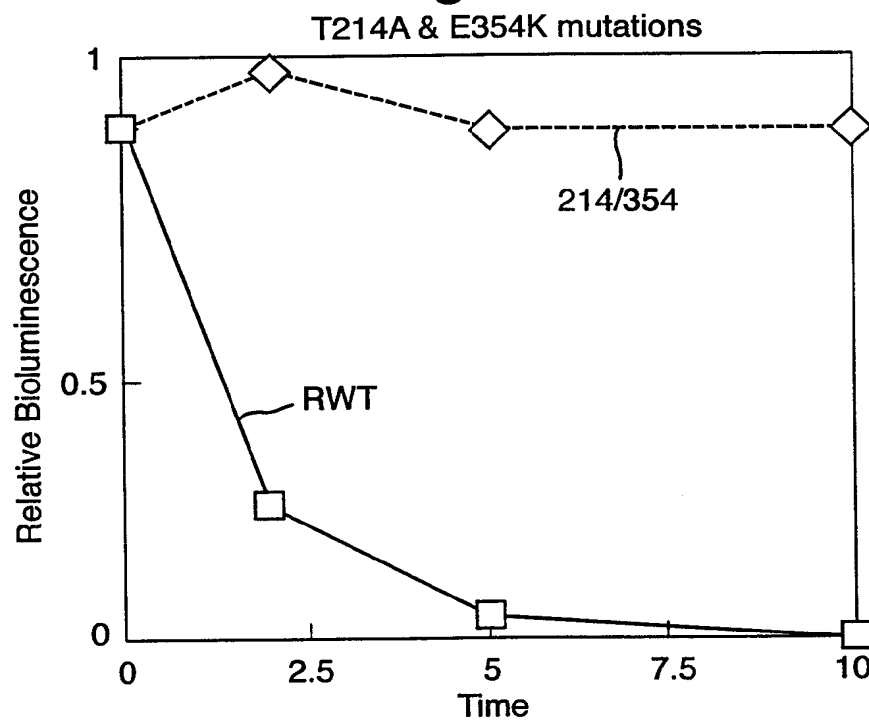


Fig.3b.



5/8

Fig.3c.

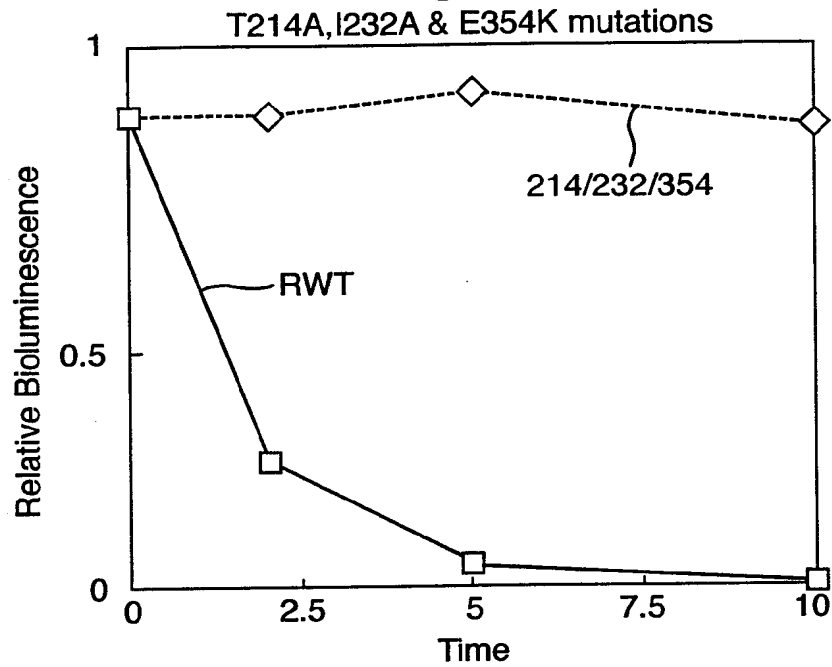


Fig.3d.

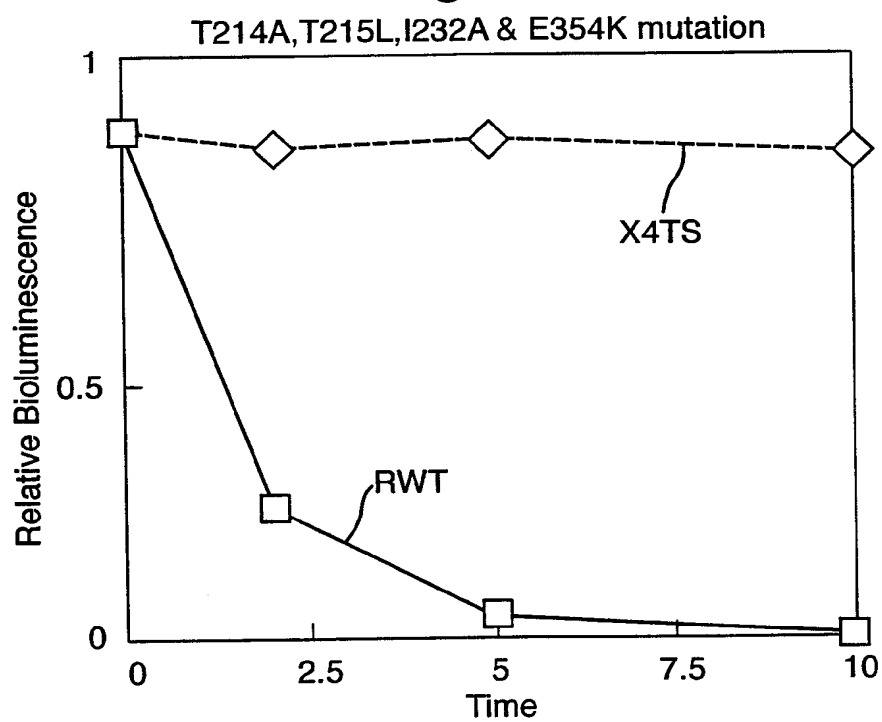


Fig.3e.

1232A mutation

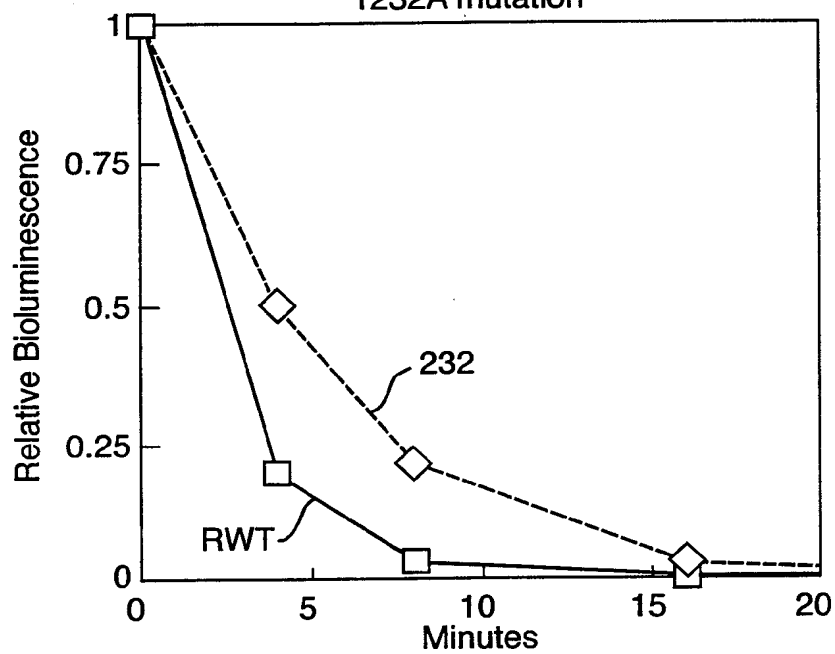


Fig.3f.

T214A & E354K mutations (44°C)

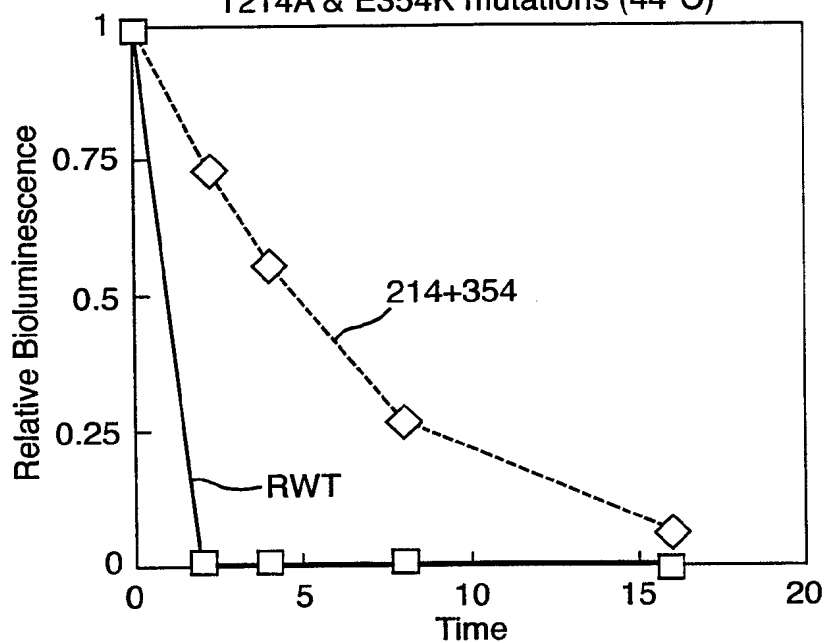


Fig.3g.

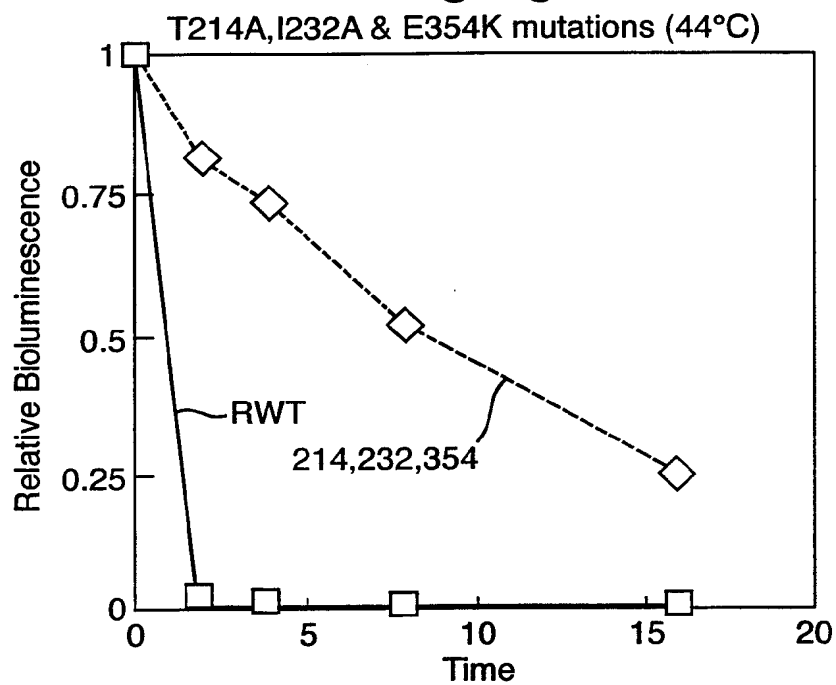


Fig.3h.

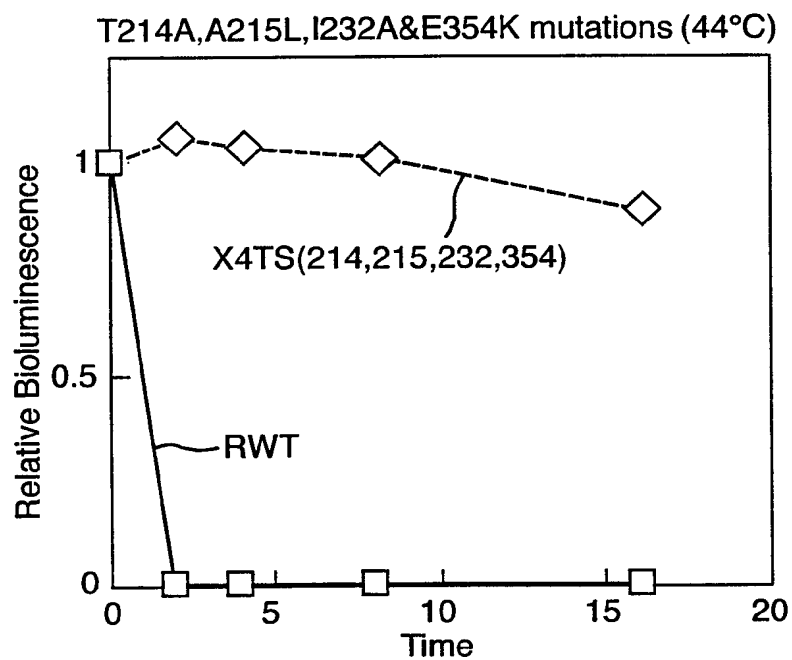


Fig.8.

CGCCGGTGAGCTCCCCGCCGCCG SACI-SENSE / 6371
 CGGCGGGCGGGAGCTCACC GGCG SACI-ANTI / 6372
 CGAACACTTCTTCATCGTTGACCGCCTTAAGTCTTTAATTAAATACAAAGG AFLII-SENSE / 6373
 CCTTTGTATTTAATTAAAGACTTAAGCGGTCAACTATGAAGAAGTGTTCCG AFLII-ANTI / 6374
 GAAAGGCCCGGCACCAGCCTATCCTCTAGAGG F14A-SENSE / 6375
 CCTCTAGCGGATAGGCTGGTGCCGGGCCCTTC F14A-ANTI / 6376
 CCATAAATTTACCGAATTCGTCGACTTCGATCGAGG C-TERM.SEQ/ 6641
 GTGTGGAATTGTGAGCGG N-TERM.SEQ / 6651
 GAGATACGCCCGGTTCTCTGG L35A-SENSE / 6652
 CCAGGAACCGCGCGTATCTC L35A-SENSE / 6653

CCCTATTTTTCATTCTGGCCAAAAGCACTG F295L-SENSE/ 9048
 GAGTGCTTTTGGCCAGGAATGAAAATAGGG F295L-ANTI / 9049
 CCGCATAGAGCTCTCTGCGTCAGATTTC T214A + A215L-SENSE / 9063
 GAATCTGACGCAGAGAGCTCTATGCGG T214A + A215L-ANTI / 9064
 GTTGACCGCTTGGGATCCTTAATTAAATAC Insertion of BamHI at G339 / 9077

GTATAGATTTGAAAAAGAGCTG E270K-SENSE / 257
 CAGCTCTTTTTCAAATCTATAC E270K-ANTI / 258
 GGCTACATACTGGAGACATAGC S420T-SENSE / 629
 GCTATGTCTCCAGTATGTAGCC S420T-ANTI / 630
 GCAGTTGCGCCCGTGAACGAC A105L-SENSE / 790
 GTCGTTACGGGCGCAACTGC A105L-ANTI / 791
 CAAATCATTCGGGGTACTGCGATTTTAAG D234G-SENSE / 792
 CTTAAAATCGCAGTACCCGGAATGATTG D234G-ANTI / 793

CCGCATAGAACTCTCTGCGTCAGATTTC A215L-SENSE / 7726
 GAATCTGACGCAGAGAGTTCTATGCGC A215L-ANTI / 7727
 CTGATTACACCCAAGGGGGATG E354K-SENSE / 7792
 CATCCCCCTTGGGTGTAATCAG E354K-ANTI / 7793
 cccttcgcatagannngcctgcgtcagt T214N-Sense / 8202
 actgacgcaggeNNNtctatcggaaggg T214N-Anti / 82033

GCAATCAAATCGCTCCGGATACTGC I232A-SENSE / 6911
 GCAGTATCCGGAGCGATTGATTGC I232A-ANTI / 6912

CCATTCCATCAAGGTTTTGG H245Q-SENSE / 9128
 CCAAAACCTTGATGGAATGG H245Q-ANTI / 9129